

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: DIXIT, VISHVA M.
O'ROURKE, KAREN

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING
FAS-ASSOCIATED APOPTOSIS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Morrison & Foerster
(B) STREET: 755 Page Mill Road
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/443,982
(B) FILING DATE: 18-MAY-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Konski, Antoinette F.
(B) REGISTRATION NUMBER: 34,202
(C) REFERENCE/DOCKET NUMBER: 20344-21070.20

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (415) 813-5600
(B) TELEFAX: (415) 494-0792
(C) TELEX: 706141 MRSNFOERS SFO

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

B1
control

(B) LOCATION: 130..756

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 4..6

(D) OTHER INFORMATION: /note= "An in-frame stop codon 130 base pairs upstream of the initiator methionine"

(ix) FEATURE:

(A) NAME/KEY: polyA_signal

(B) LOCATION: 1636..1641

(D) OTHER INFORMATION: /note= "Potential poly(A) adenylation signal"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 198..753

(D) OTHER INFORMATION: /note= "Clone-15; 5' end of FADD"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 249..753

(D) OTHER INFORMATION: /note= "Clone-8; 5' end of FADD"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 177..658

(D) OTHER INFORMATION: /note= "Death Domain of FADD"

(ix) FEATURE:

(A) NAME/KEY: mutation

(B) LOCATION: replace(490..492, "aay")

(D) OTHER INFORMATION: /note= "For FADDmt: sequence is altered to either AAT or AAC and the codon from Val to Asn"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: group(250..753, 232..753)

(D) OTHER INFORMATION: /note= "Codons can comprise C-terminal polypeptide fragments of FADD"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 253..753

(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-2"

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 310..753

(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-3"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 367..753
 (D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-4"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 131..504
 (D) OTHER INFORMATION: /note= "Codons can comprise an N-terminal half polypeptide fragment of FADD designated N-FADD"

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION: 133..501
 (D) OTHER INFORMATION: /note= "Codons can comprise an N-terminal half polypeptide fragment of FADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG	60
GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA	120
GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC	168
Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser	
1 5 10	
AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG	216
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly	
15 20 25	
CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC	264
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu	
30 35 40 45	
TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG	312
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu	
50 55 60	
CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG	360
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg	
65 70 75	
CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG	408
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly	
80 85 90	
GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG	456
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly	
95 100 105	

AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG	504
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys	
110 115 120 125	
ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG	552
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val	
130 135 140	
CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA	600
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr	
145 150 155	
GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG	648
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val	
160 165 170	
GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG	696
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg	
175 180 185	
AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC	744
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser	
190 195 200 205	
GAA GCG TCC TGA TGGGCCGCTG CTTTGCGCTG GTGGACCACA GGCATCTACA	796
Glu Ala Ser *	
CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA	856
GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC	916
TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG	976
ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG	1036
AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC	1096
GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA	1156
TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC	1216
CCTGCAGTTG GCAGAAAGGA TGTTTTGTCC CATTTCTTGT GAGGCCACCG GGACAGACCT	1276
GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG	1336
GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCTGTGT GAGTTGAGTC TCCTCTCTGA	1396
GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG	1456
CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG	1516
CAATTCTACA GTTTCTTACT GTTTTGATC AAAATCACTA TCTTTCTGAT AACAGAATTG	1576

CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA 1636
TTAAAA 1642

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Pro	Phe	Leu	Val	Leu	Leu	His	Ser	Val	Ser	Ser	Ser	Leu	Ser	1	5	10	15
Ser	Ser	Glu	Leu	Thr	Glu	Leu	Lys	Phe	Leu	Cys	Leu	Gly	Arg	Val	Gly	20	25	30	
Lys	Arg	Lys	Leu	Glu	Arg	Val	Gln	Ser	Gly	Leu	Asp	Leu	Phe	Ser	Met	35	40	45	
Leu	Leu	Glu	Gln	Asn	Asp	Leu	Glu	Pro	Gly	His	Thr	Glu	Leu	Leu	Arg	50	55	60	
Glu	Leu	Leu	Ala	Ser	Leu	Arg	Arg	His	Asp	Leu	Leu	Arg	Arg	Val	Asp	65	70	75	80
Asp	Phe	Glu	Ala	Gly	Ala	Ala	Ala	Gly	Ala	Ala	Pro	Gly	Glu	Glu	Asp	85	90	95	
Leu	Cys	Ala	Ala	Phe	Asn	Val	Ile	Cys	Asp	Asn	Val	Gly	Lys	Asp	Trp	100	105	110	
Arg	Arg	Leu	Ala	Arg	Gln	Leu	Lys	Val	Ser	Asp	Thr	Lys	Ile	Asp	Ser	115	120	125	
Ile	Glu	Asp	Arg	Tyr	Pro	Arg	Asn	Leu	Thr	Glu	Arg	Val	Arg	Glu	Ser	130	135	140	
Leu	Arg	Ile	Trp	Lys	Asn	Thr	Glu	Lys	Glu	Asn	Ala	Thr	Val	Ala	His	145	150	155	160
Leu	Val	Gly	Ala	Leu	Arg	Ser	Cys	Gln	Met	Asn	Leu	Val	Ala	Asp	Leu	165	170	175	
Val	Gln	Glu	Val	Gln	Gln	Ala	Arg	Asp	Leu	Gln	Asn	Arg	Ser	Gly	Ala	180	185	190	
Met	Ser	Pro	Met	Ser	Trp	Asn	Ser	Asp	Ala	Ser	Thr	Ser	Glu	Ala	Ser	195	200	205	

*

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Val is replaced by Asn for the point mutant hFADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp	Trp	Arg	Arg	Leu	Ala	Arg	Gln	Leu	Lys	Val	Ser	Asp	Thr	Lys	Ile
1				5				10						15	
Asp	Ser	Ile	Glu	Asp	Arg	Tyr	Pro	Arg	Asn	Leu	Thr	Glu	Arg	Val	Arg
			20					25					30		
Glu	Ser	Leu	Arg	Ile	Trp	Lys	Asn	Thr	Glu	Lys	Glu	Asn	Ala	Thr	Val
		35					40					45			
Ala	His	Leu	Val	Gly	Ala	Leu	Arg	Ser	Cys	Gln	Met	Asn	Leu	Val	Ala
	50					55					60				
Asp	Leu	Val	Gln	Glu	Val										
65				70											

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Ile is replaced by Asn for the point mutant rFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```

Asp Ala Lys Lys Phe Ala Arg Gln His Lys Ile Pro Glu Ser Lys Ile
1           5           10           15

Asp Glu Ile Glu His Asn Ser Pro Gln Asp Ala Ala Glu Gln Lys Ile
          20           25           30

Gln Leu Leu Gln Cys Trp Tyr Gln Ser His Gly Lys Thr Gly Ala Cys
          35           40           45

Gln Ala Leu Ile Gln Gly Leu Arg Lys Ala Asn Arg Cys Asp Ile Ala
          50           55           60

Glu Glu Ile Gln Ala Met
65           70

```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Val is replaced by Asn for the point mutant hFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```

Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile
1           5           10           15

Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val
          20           25           30

Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr
          35           40           45

Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala
          50           55           60

Glu Lys Ile Gln Thr Ile
65           70

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /note= "Leu is replaced by Asn for the point mutant hTNFR-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg	Trp	Lys	Glu	Phe	Val	Arg	Arg	Leu	Gly	Leu	Ser	Asp	His	Glu	Ile
1				5					10					15	
Asp	Arg	Leu	Glu	Leu	Gln	Asn	Gly	Arg	Cys	Leu	Arg	Glu	Ala	Gln	Tyr
			20					25					30		
Ser	Met	Leu	Ala	Thr	Trp	Arg	Arg	Arg	Thr	Pro	Arg	Arg	Glu	Ala	Thr
			35					40					45		
Leu	Glu	Leu	Leu	Gly	Arg	Val	Leu	Arg	Asp	Met	Asp	Leu	Leu	Gly	Cys
	50					55					60				
Leu	Glu	Asp	Ile	Glu	Glu										
65					70										

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Tyr	Pro	Tyr	Asp	Val	Pro	Asp	Tyr	Ala
1				5				

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Thr Tyr Arg Tyr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAGCCTGGTA CCATGCTGGG CATCTGGACC CTCCTACCTC TGGTTCTTAC GTCTGTTGCT 60

AGATTATCGT CCAAAGACTA CAAGGACGAC GATGACAAGA GTGTTAATGC CCAAGTC 117
